

SEQUENCE LISTING

<110> Innovations Foundation

<120> Recombinant BCG Strains Expressing Alanine Dehydrogenase,
Serine dehydratase and/or Glutamine Synthetase as TB Vaccines

<130>

<150> US 60/372,450

<151> 2002-04-16

<160> 14

<170> PatentIn version 3.0

<210> 1

<211> 1116

<212> DNA

<213> Mycobacterium tuberculosis

<220>

<221> CDS

<222> (1)..(1116)

<223> Sequence is identical to GenBank entries GI:3089350 and MTU92472

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gcc atc acc ccg gcc ggc gtc gcg gaa cta acc cgt cgt ggc cat gag      96
Ala Ile Thr Pro Ala Gly Val Ala Glu Leu Thr Arg Arg Gly His Glu
20          25          30

gtg ctc atc cag gca ggt gcc gga gag ggc tcg gct atc acc gac gcg      144
Val Leu Ile Gln Ala Gly Ala Gly Glu Gly Ser Ala Ile Thr Asp Ala
35          40          45

gat ttc aag gcg gca ggc gcg caa ctg gtc ggc acc gcc gac cag gtg      192
Asp Phe Lys Ala Ala Gly Ala Gln Leu Val Gly Thr Ala Asp Gln Val
50          55          60

tgg gcc gac gct gat tta ttg ctc aag gtc aaa gaa ccg ata gcg gcg      240
Trp Ala Asp Ala Asp Leu Leu Leu Lys Val Lys Glu Pro Ile Ala Ala
65          70          75          80

gaa tac ggc cgc ctg cga cac ggg cag atc ttg ttc acg ttc ttg cat      288
Glu Tyr Gly Arg Leu Arg His Gly Gln Ile Leu Phe Thr Phe Leu His
85          90          95

ttg gcc gcg tca cgt gct tgc acc gat gcg ttg ttg gat tcc ggc acc      336
Leu Ala Ala Ser Arg Ala Cys Thr Asp Ala Leu Leu Asp Ser Gly Thr
100         105         110

acg tca att gcc tac gag acc gtc cag acc gcc gac ggc gca cta ccc      384

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Thr	Val	Thr	Val	Leu	Asp	Ile	Asn	Ile	Asp	Lys	Leu	Arg	Gln	Leu	Asp		
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Ala	Glu	Phe	Cys	Gly	Arg	Ile	His	Thr	Arg	Tyr	Ser	Ser	Ala	Tyr	Glu		
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gtg	cca	ggc	gcc	aag	gca	ccc	aaa	tta	gtc	tcg	aat	tca	ctt	gtc	gcg	768	
Val	Pro	Gly	Ala	Lys	Ala	Pro	Lys	Leu	Val	Ser	Asn	Ser	Leu	Val	Ala		
				245					250					255			
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His	Met	Lys	Pro	Gly	Ala	Val	Leu	Val	Asp	Ile	Ala	Ile	Asp	Gln	Gly		
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Val Leu Ala
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<210> 2
<211> 371
<212> PRT
<213> Mycobacterium tuberculosis

<220>
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<223> Sequence is identical to SwissProt entry SP:DHA_MYCTU

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          20          25          30

Val Leu Ile Gln Ala Gly Ala Gly Glu Gly Ser Ala Ile Thr Asp Ala
          35          40          45

Asp Phe Lys Ala Ala Gly Ala Gln Leu Val Gly Thr Ala Asp Gln Val
          50          55          60

Trp Ala Asp Ala Asp Leu Leu Leu Lys Val Lys Glu Pro Ile Ala Ala
65          70          75          80

Glu Tyr Gly Arg Leu Arg His Gly Gln Ile Leu Phe Thr Phe Leu His
          85          90          95

Leu Ala Ala Ser Arg Ala Cys Thr Asp Ala Leu Leu Asp Ser Gly Thr
          100          105          110

Thr Ser Ile Ala Tyr Glu Thr Val Gln Thr Ala Asp Gly Ala Leu Pro
          115          120          125

Leu Leu Ala Pro Met Ser Glu Val Ala Gly Arg Leu Ala Ala Gln Val
          130          135          140

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Gly Ala Tyr His Leu Met Arg Thr Gln Gly Gly Arg Gly Val Leu Met
 145 150 155 160

Gly Gly Val Pro Gly Val Glu Pro Ala Asp Val Val Val Ile Gly Ala
 165 170 175

Gly Thr Ala Gly Tyr Asn Ala Ala Arg Ile Ala Asn Gly Met Gly Ala
 180 185 190

Thr Val Thr Val Leu Asp Ile Asn Ile Asp Lys Leu Arg Gln Leu Asp
 195 200 205

Ala Glu Phe Cys Gly Arg Ile His Thr Arg Tyr Ser Ser Ala Tyr Glu
 210 215 220

Leu Glu Gly Ala Val Lys Arg Ala Asp Leu Val Ile Gly Ala Val Leu
 225 230 235 240

Val Pro Gly Ala Lys Ala Pro Lys Leu Val Ser Asn Ser Leu Val Ala
 245 250 255

His Met Lys Pro Gly Ala Val Leu Val Asp Ile Ala Ile Asp Gln Gly
 260 265 270

Gly Cys Phe Glu Gly Ser Arg Pro Thr Thr Tyr Asp His Pro Thr Phe
 275 280 285

Ala Val His Asp Thr Leu Phe Tyr Cys Val Ala Asn Met Pro Ala Ser
 290 295 300

Val Pro Lys Thr Ser Thr Tyr Ala Leu Thr Asn Ala Thr Met Pro Tyr
 305 310 315 320

Val Leu Glu Leu Ala Asp His Gly Trp Arg Ala Ala Cys Arg Ser Asn
 325 330 335

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Val Leu Ala
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<213> Mycobacterium bovis

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<221> CDS
<222> (1)..(399)

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Ala Ile Thr Pro Ala Gly Val Ala Glu Leu Thr Arg Arg Gly His Glu
20 25 30
gtg ctc atc cag gca ggt gcc gga gag ggc tcg gct atc acc gac gcg 144
Val Leu Ile Gln Ala Gly Ala Gly Glu Gly Ser Ala Ile Thr Asp Ala
35 40 45
gat ttc aag gcg gca ggc gcg caa ctg gtc ggc acc gcc gac cag gtg 192
Asp Phe Lys Ala Ala Gly Ala Gln Leu Val Gly Thr Ala Asp Gln Val
50 55 60
tgg gcc gac gct gat tta ttg ctc aag gtc aaa gaa ccg ata gcg gcg 240
Trp Ala Asp Ala Asp Leu Leu Leu Lys Val Lys Glu Pro Ile Ala Ala
65 70 75 80
gaa tac ggc cgc ctg cga cac ggg cga tct tgt tca cgt tct tgc att 288
Glu Tyr Gly Arg Leu Arg His Gly Arg Ser Cys Ser Arg Ser Cys Ile
85 90 95
tgg ccg cgt cac gtg ctt gca ccg atg cgt tgt tgg att ccg gca cca 336
Trp Pro Arg His Val Leu Ala Pro Met Arg Cys Trp Ile Pro Ala Pro
100 105 110
cgt caa ttg cct acg aga ccg tcc aga ccg ccg acg gcg cac tac ccc 384
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Cys Leu Pro Arg
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<212> PRT
<213> Mycobacterium bovis

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Val Leu Ile Gln Ala Gly Ala Gly Glu Gly Ser Ala Ile Thr Asp Ala
35 40 45

Asp Phe Lys Ala Ala Gly Ala Gln Leu Val Gly Thr Ala Asp Gln Val
50 55 60

Trp Ala Asp Ala Asp Leu Leu Lys Val Lys Glu Pro Ile Ala Ala
65 70 75 80

Glu Tyr Gly Arg Leu Arg His Gly Arg Ser Cys Ser Arg Ser Cys Ile
85 90 95

Trp Pro Arg His Val Leu Ala Pro Met Arg Cys Trp Ile Pro Ala Pro
100 105 110

Arg Gln Leu Pro Thr Arg Pro Ser Arg Pro Pro Thr Ala His Tyr Pro
115 120 125

Cys Leu Pro Arg
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<210> 5
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<212> DNA
<213> Mycobacterium tuberculosis

<220>
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<222> (1)..(1386)
<223> Sequence is identical to the complement of nucleotides 13172-14551
of GenBank entry GB:MTV030 [AL021428]
Sequence is identical to the complement of nucleotides 13195-14580
of GenBank entry GB:AE006919

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agt tcc cac acc gtg gga ccg atg cgc gcg gca aac cag ttc gta gtt 96
Ser Ser His Thr Val Gly Pro Met Arg Ala Ala Asn Gln Phe Val Val

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gat ctg ttc ggc tcg ctc gcg gcc acc gga gcc ggt cat ggc acc atg Asp Leu Phe Gly Ser Leu Ala Ala Thr Gly Ala Gly His Gly Thr Met 50 55 60			192
tcg gcg ata ttg ctg ggg ctg gaa ggc tgc cag cca gaa acg att acc Ser Ala Ile Leu Leu Gly Leu Glu Gly Cys Gln Pro Glu Thr Ile Thr 65 70 75 80			240
acc gaa cac aag gaa cgc cgg ctc gcc gag atc gca gcg tcc ggc gtg Thr Glu His Lys Glu Arg Arg Leu Ala Glu Ile Ala Ala Ser Gly Val 85 90 95			288
acg cga atc ggc ggt gtc att ccg gtc ccg ctg acc gag cgt gat atc Thr Arg Ile Gly Gly Val Ile Pro Val Pro Leu Thr Glu Arg Asp Ile 100 105 110			336
gac ctg cat ccc gac atc gtt ctg cca acg cat ccc aac gga atg acg Asp Leu His Pro Asp Ile Val Leu Pro Thr His Pro Asn Gly Met Thr 115 120 125			384
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 Pro Glu Phe Ala Glu Asp Trp Val Asn Leu Val Ala Leu Ala Val Asn
 260 265 270

gag gag aac gcc tcc ggt ggg cgc gtc gtc acc gcc ccg acc aac ggt 864
 Glu Glu Asn Ala Ser Gly Gly Arg Val Val Thr Ala Pro Thr Asn Gly
 275 280 285

gcc gcc ggc atc gtg ccg gcg gtc ctg cac tac gca atc cac tac acg 912
 Ala Ala Gly Ile Val Pro Ala Val Leu His Tyr Ala Ile His Tyr Thr
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tcg gcc ggc gcg ggg gac ccc gac gat gtc acc gtg cga ttc ctg ctc 960
 Ser Ala Gly Ala Gly Asp Pro Asp Asp Val Thr Val Arg Phe Leu Leu
 305 310 315 320

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 Thr Ala Gly Ala Ile Gly Ser Leu Phe Lys Glu Arg Ala Ser Ile Ser
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 340 345 350

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 355 360 365

gaa aac gcc gcc gag atc gcc atg gaa cac agc ctc ggc ctg acc tgt 1152
 Glu Asn Ala Ala Glu Ile Ala Met Glu His Ser Leu Gly Leu Thr Cys
 370 375 380

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 Asp Pro Ile Ala Gly Leu Val Gln Ile Pro Cys Ile Glu Arg Asn Ala
 385 390 395 400

att tcc gcc ggc aag gcc atc aac gcc gca cgg atg gca ttg cgc ggc 1248
 Ile Ser Ala Gly Lys Ala Ile Asn Ala Ala Arg Met Ala Leu Arg Gly
 405 410 415

gac ggc atc cat cgc gtc acc ctc gac cag gtc atc gac acc atg cgc 1296
 Asp Gly Ile His Arg Val Thr Leu Asp Gln Val Ile Asp Thr Met Arg
 420 425 430

gcc acc ggc gcg gac atg cac acc aag tac aag gaa acc tcg gcc ggc 1344
 Ala Thr Gly Ala Asp Met His Thr Lys Tyr Lys Glu Thr Ser Ala Gly
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<210> 6
 <211> 461
 <212> PRT

<213> Mycobacterium tuberculosis

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<221>

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<223> Sequence is identical to SwissProt entry SP:SDHL_MYCTU
Sequence is identical to GenBank entries GP:AE006919_13
and GP:MTV030_11

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35 40 45

Asp Leu Phe Gly Ser Leu Ala Ala Thr Gly Ala Gly His Gly Thr Met
50 55 60

Ser Ala Ile Leu Leu Gly Leu Glu Gly Cys Gln Pro Glu Thr Ile Thr
65 70 75 80

Thr Glu His Lys Glu Arg Arg Leu Ala Glu Ile Ala Ala Ser Gly Val
85 90 95

Thr Arg Ile Gly Gly Val Ile Pro Val Pro Leu Thr Glu Arg Asp Ile
100 105 110

Asp Leu His Pro Asp Ile Val Leu Pro Thr His Pro Asn Gly Met Thr
115 120 125

Phe Thr Ala Ala Gly Pro His Gly Arg Val Leu Ala Thr Glu Thr Tyr
130 135 140

Phe Ser Val Gly Gly Gly Phe Ile Val Thr Glu Gln Thr Ser Gly Asn
145 150 155 160

Ser Gly Gln His Pro Cys Ser Val Ala Leu Pro Tyr Val Ser Ala Gln
165 170 175

Glu Leu Leu Asp Ile Cys Asp Arg Leu Asp Val Ser Ile Ser Glu Ala
180 185 190

Ala Leu Arg Asn Glu Thr Cys Cys Arg Thr Glu Asn Glu Val Arg Ala
 195 200 205

Ala Leu Leu His Leu Arg Asp Val Met Val Glu Cys Glu Gln Arg Ser
 210 215 220

Ile Ala Arg Glu Gly Leu Leu Pro Gly Gly Leu Arg Val Arg Arg Arg
 225 230 235 240

Ala Lys Val Trp Tyr Asp Arg Leu Asn Ala Glu Asp Pro Thr Arg Lys
 245 250 255

Pro Glu Phe Ala Glu Asp Trp Val Asn Leu Val Ala Leu Ala Val Asn
 260 265 270

Glu Glu Asn Ala Ser Gly Gly Arg Val Val Thr Ala Pro Thr Asn Gly
 275 280 285

Ala Ala Gly Ile Val Pro Ala Val Leu His Tyr Ala Ile His Tyr Thr
 290 295 300

Ser Ala Gly Ala Gly Asp Pro Asp Asp Val Thr Val Arg Phe Leu Leu
 305 310 315 320

Thr Ala Gly Ala Ile Gly Ser Leu Phe Lys Glu Arg Ala Ser Ile Ser
 325 330 335

Gly Ala Glu Val Gly Cys Gln Gly Glu Val Gly Ser Ala Ala Ala Met
 340 345 350

Ala Ala Ala Gly Leu Ala Glu Ile Leu Gly Gly Thr Pro Arg Gln Val
 355 360 365

Glu Asn Ala Ala Glu Ile Ala Met Glu His Ser Leu Gly Leu Thr Cys
 370 375 380

Asp Pro Ile Ala Gly Leu Val Gln Ile Pro Cys Ile Glu Arg Asn Ala
 385 390 395 400

Ile Ser Ala Gly Lys Ala Ile Asn Ala Ala Arg Met Ala Leu Arg Gly
 405 410 415

Asp Gly Ile His Arg Val Thr Leu Asp Gln Val Ile Asp Thr Met Arg
 420 425 430

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<210> 7
 <211> 1437
 <212> DNA
 <213> Mycobacterium tuberculosis

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 <221> CDS
 <222> (1)..(1437)
 <223> Sequence is identical to GenBank entry GB:MTU87280 [U87280]
 Sequence is identical to nucleotides 163-1599 of GenBank
 entry GB:MTCY427 [Z70692]
 Sequence is identical to nucleotides 93-1529 of GenBank entry GB:AE00707

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 Lys Val Glu Tyr Val Asp Val Arg Phe Cys Asp Leu Pro Gly Ile Met
 20 25 30

 cag cac ttc acg att ccg gct tcg gcc ttt gac aag agc gtg ttt gac 144
 Gln His Phe Thr Ile Pro Ala Ser Ala Phe Asp Lys Ser Val Phe Asp
 35 40 45

 gac ggc ttg gcc ttt gac ggc tcg tcg att cgc ggg ttc cag tcg atc 192
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 50 55 60

 cac gaa tcc gac atg ttg ctt ctt ccc gat ccc gag acg gcg cgc atc 240
 His Glu Ser Asp Met Leu Leu Leu Pro Asp Pro Glu Thr Ala Arg Ile
 65 70 75 80

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 85 90 95

 gac ccg ttc acc ctg gag ccg tac tcc cgc gac ccg cgc aac atc gcc 336
 Asp Pro Phe Thr Leu Glu Pro Tyr Ser Arg Asp Pro Arg Asn Ile Ala
 100 105 110

 cgc aag gcc gag aac tac ctg atc agc act ggc atc gcc gac acc gca 384

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Tyr Phe Gly Ala Glu Ala Glu Phe Tyr Ile Phe Asp Ser Val Ser Phe	
130 135 140	
gac tcg cgc gcc aac ggc tcc ttc tac gag gtg gac gcc atc tcg ggg	480
Asp Ser Arg Ala Asn Gly Ser Phe Tyr Glu Val Asp Ala Ile Ser Gly	
145 150 155 160	
tgg tgg aac acc ggc gcg gcg acc gag gcc gac ggc agt ccc aac cgg	528
Trp Trp Asn Thr Gly Ala Ala Thr Glu Ala Asp Gly Ser Pro Asn Arg	
165 170 175	
ggc tac aag gtc cgc cac aag ggc ggg tat ttc cca gtg gcc ccc aac	576
Gly Tyr Lys Val Arg His Lys Gly Gly Tyr Phe Pro Val Ala Pro Asn	
180 185 190	
gac caa tac gtc gac ctg cgc gac aag atg ctg acc aac ctg atc aac	624
Asp Gln Tyr Val Asp Leu Arg Asp Lys Met Leu Thr Asn Leu Ile Asn	
195 200 205	
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Gln Ala Glu Ile Asn Tyr Gln Phe Asn Ser Leu Leu His Ala Ala Asp	
225 230 235 240	
gac atg cag ttg tac aag tac atc atc aag aac acc gcc tgg cag aac	768
Asp Met Gln Leu Tyr Lys Tyr Ile Ile Lys Asn Thr Ala Trp Gln Asn	
245 250 255	
ggc aaa acg gtc acg ttc atg ccc aag ccg ctg ttc ggc gac aac ggg	816
Gly Lys Thr Val Thr Phe Met Pro Lys Pro Leu Phe Gly Asp Asn Gly	
260 265 270	
tcc ggc atg cac tgt cat cag tcg ctg tgg aag gac ggg gcc ccg ctg	864
Ser Gly Met His Cys His Gln Ser Leu Trp Lys Asp Gly Ala Pro Leu	
275 280 285	
atg tac gac gag acg ggt tat gcc ggt ctg tcg gac acg gcc cgt cat	912
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290 295 300	
tac atc ggc ggc ctg tta cac cac gcg ccg tcg ctg ctg gcc ttc acc	960
Tyr Ile Gly Gly Leu Leu His His Ala Pro Ser Leu Leu Ala Phe Thr	
305 310 315 320	
aac ccg acg gtg aac tcc tac aag ccg ctg gtt ccc ggt tac gag gcc	1008
Asn Pro Thr Val Asn Ser Tyr Lys Arg Leu Val Pro Gly Tyr Glu Ala	
325 330 335	
ccg atc aac ctg gtc tat agc cag cgc aac ccg tcg gca tgc gtg cgc	1056
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<210>      8
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<212>     PRT
<213>  Mycobacterium tuberculosis
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<220>
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<223> Sequence is identical to SwissProt entry SP:GLN1_MYCTU
Sequence is identical to PIR entry PIR:H70775
Sequence is identical to PRF entry PRF:2323405A
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Gln His Phe Thr Ile Pro Ala Ser Ala Phe Asp Lys Ser Val. Phe Asp

35	40	45
Asp Gly Leu Ala Phe Asp Gly Ser Ser Ile Arg Gly Phe Gln Ser Ile		
50	55	60
His Glu Ser Asp Met Leu Leu Leu Pro Asp Pro Glu Thr Ala Arg Ile		
65	70	75
Asp Pro Phe Arg Ala Ala Lys Thr Leu Asn Ile Asn Phe Phe Val His		
85	90	95
Asp Pro Phe Thr Leu Glu Pro Tyr Ser Arg Asp Pro Arg Asn Ile Ala		
100	105	110
Arg Lys Ala Glu Asn Tyr Leu Ile Ser Thr Gly Ile Ala Asp Thr Ala		
115	120	125
Tyr Phe Gly Ala Glu Ala Glu Phe Tyr Ile Phe Asp Ser Val Ser Phe		
130	135	140
Asp Ser Arg Ala Asn Gly Ser Phe Tyr Glu Val Asp Ala Ile Ser Gly		
145	150	155
Trp Trp Asn Thr Gly Ala Ala Thr Glu Ala Asp Gly Ser Pro Asn Arg		
165	170	175
Gly Tyr Lys Val Arg His Lys Gly Gly Tyr Phe Pro Val Ala Pro Asn		
180	185	190
Asp Gln Tyr Val Asp Leu Arg Asp Lys Met Leu Thr Asn Leu Ile Asn		
195	200	205
Ser Gly Phe Ile Leu Glu Lys Gly His His Glu Val Gly Ser Gly Gly		
210	215	220
Gln Ala Glu Ile Asn Tyr Gln Phe Asn Ser Leu Leu His Ala Ala Asp		
225	230	235
Asp Met Gln Leu Tyr Lys Tyr Ile Ile Lys Asn Thr Ala Trp Gln Asn		
245	250	255
Gly Lys Thr Val Thr Phe Met Pro Lys Pro Leu Phe Gly Asp Asn Gly		
260	265	270

Ser Gly Met His Cys His Gln Ser Leu Trp Lys Asp Gly Ala Pro Leu
 275 280 285

Met Tyr Asp Glu Thr Gly Tyr Ala Gly Leu Ser Asp Thr Ala Arg His
 290 295 300

Tyr Ile Gly Gly Leu Leu His His Ala Pro Ser Leu Leu Ala Phe Thr
 305 310 315 320

Asn Pro Thr Val Asn Ser Tyr Lys Arg Leu Val Pro Gly Tyr Glu Ala
 325 330 335

Pro Ile Asn Leu Val Tyr Ser Gln Arg Asn Arg Ser Ala Cys Val Arg
 340 345 350

Ile Pro Ile Thr Gly Ser Asn Pro Lys Ala Lys Arg Leu Glu Phe Arg
 355 360 365

Ser Pro Asp Ser Ser Gly Asn Pro Tyr Leu Ala Phe Ser Ala Met Leu
 370 375 380

Met Ala Gly Leu Asp Gly Ile Lys Asn Lys Ile Glu Pro Gln Ala Pro
 385 390 395 400

Val Asp Lys Asp Leu Tyr Glu Leu Pro Pro Glu Glu Ala Ala Ser Ile
 405 410 415

Pro Gln Thr Pro Thr Gln Leu Ser Asp Val Ile Asp Arg Leu Glu Ala
 420 425 430

Asp His Glu Tyr Leu Thr Glu Gly Gly Val Phe Thr Asn Asp Leu Ile
 435 440 445

Glu Thr Trp Ile Ser Phe Lys Arg Glu Asn Glu Ile Glu Pro Val Asn
 450 455 460

Ile Arg Pro His Pro Tyr Glu Phe Ala Leu Tyr Tyr Asp Val
 465 470 475

<210> 9
 <211> 1341
 <212> DNA

<213> Mycobacterium tuberculosis

<220>

<221> CDS

<222> (1)..(1341)

<223> Sequence is identical to complement of nucleotides 4950-6290 of GenBank entry GB:MTCY427 [Z70692]

Sequence is identical to complement of nucleotides 4880-6220 of GenBank entry GB:AE007073

<400> 9

atg gac cga cag aag gaa ttc gtt ctt cgt acc ctg gaa gaa cgc gac	48
Met Asp Arg Gln Lys Glu Phe Val Leu Arg Thr Leu Glu Glu Arg Asp	
1 5 10 15	
atc cgc ttc gtc cgg ctg tgg ttc aca gac gtg ctc ggt ttc ctc aag	96
Ile Arg Phe Val Arg Leu Trp Phe Thr Asp Val Leu Gly Phe Leu Lys	
20 25 30	
tcg gtc gcc atc gcc cca gcc gaa ctc gag ggc gcc ttc gag gaa ggc	144
Ser Val Ala Ile Ala Pro Ala Glu Leu Glu Gly Ala Phe Glu Glu Gly	
35 40 45	
atc ggc ttc gac gga tcc tcg atc gag ggc ttt gcg cgg gtc tcg gaa	192
Ile Gly Phe Asp Gly Ser Ser Ile Glu Gly Phe Ala Arg Val Ser Glu	
50 55 60	
tcc gat acg gtg gcg cac ccg gac ccg tcg acc ttc cag gtg ctg ccc	240
Ser Asp Thr Val Ala His Pro Asp Pro Ser Thr Phe Gln Val Leu Pro	
65 70 75 80	
tgg gcc acc agt tcc ggc cac cac cac tca gcg cgg atg ttt tgc gac	288
Trp Ala Thr Ser Ser Gly His His His Ser Ala Arg Met Phe Cys Asp	
85 90 95	
atc acc atg ccg gac ggc tcg ccg tcg tgg gcg gac ccg cgg cac gtg	336
Ile Thr Met Pro Asp Gly Ser Pro Ser Trp Ala Asp Pro Arg His Val	
100 105 110	
ttg cgg cgg cag ctg acg aag gcc ggc gaa ctc ggc ttc tcc tgc tac	384
Leu Arg Arg Gln Leu Thr Lys Ala Gly Glu Leu Gly Phe Ser Cys Tyr	
115 120 125	
gtg cat ccc gaa atc gag ttc ttc ctg ctc aag ccc gga ccc gag gac	432
Val His Pro Glu Ile Glu Phe Phe Leu Leu Lys Pro Gly Pro Glu Asp	
130 135 140	
ggg tcg gtg ccc gtc ccg gtc gac aac gcc ggc tat ttc gac caa gcg	480
Gly Ser Val Pro Val Pro Val Asp Asn Ala Gly Tyr Phe Asp Gln Ala	
145 150 155 160	
gtg cac gac tcc gcc ttg aac ttt cgc cgc cac gcg atc gat gcc ctg	528
Val His Asp Ser Ala Leu Asn Phe Arg Arg His Ala Ile Asp Ala Leu	
165 170 175	
gaa ttc atg ggc atc tcg gtg gag ttc agc cat cac gaa ggc gca ccc	576

Glu Phe Met Gly Ile Ser Val Glu Phe Ser His His Glu Gly Ala Pro	
180 185 190	
ggc cag cag gag atc gac ctg cgg ttt gcc gac gct ctg tcg atg gct	624
Gly Gln Gln Glu Ile Asp Leu Arg Phe Ala Asp Ala Leu Ser Met Ala	
195 200 205	
gac aac gtg atg acc ttc cgc tac gtc atc aaa gaa gtc gcg ctg gaa	672
Asp Asn Val Met Thr Phe Arg Tyr Val Ile Lys Glu Val Ala Leu Glu	
210 215 220	
gag ggc gcc cgg gcg tcg ttc atg ccc aag cca ttc ggc cag cac ccg	720
Glu Gly Ala Arg Ala Ser Phe Met Pro Lys Pro Phe Gly Gln His Pro	
225 230 235 240	
ggc tcg gcg atg cac acc cac atg agc ctg ttc gag ggt gat gtc aac	768
Gly Ser Ala Met His Thr His Met Ser Leu Phe Glu Gly Asp Val Asn	
245 250 255	
gcg ttc cac agc gct gat gat ccg ctg cag ctg tcg gaa gtg ggt aaa	816
Ala Phe His Ser Ala Asp Asp Pro Leu Gln Leu Ser Glu Val Gly Lys	
260 265 270	
tcg ttc atc gcc ggg atc ctg gag cac gct tgc gag atc agc gcg gtc	864
Ser Phe Ile Ala Gly Ile Leu Glu His Ala Cys Glu Ile Ser Ala Val	
275 280 285	
aca aat cag tgg gtc aac tct tac aag cgg ctg gtg cag ggc ggc gaa	912
Thr Asn Gln Trp Val Asn Ser Tyr Lys Arg Leu Val Gln Gly Gly Glu	
290 295 300	
gcg ccc acg gcc gcg tcg tgg ggg gcc gcc aac cga tcc gcc cta gtg	960
Ala Pro Thr Ala Ala Ser Trp Gly Ala Ala Asn Arg Ser Ala Leu Val	
305 310 315 320	
cgg gtg ccg atg tac acg ccg cac aag acc tcg tcg cgg cgg gtc gaa	1008
Arg Val Pro Met Tyr Thr Pro His Lys Thr Ser Ser Arg Arg Val Glu	
325 330 335	
gta cgc agc cct gat tcg gcg tgc aat ccc tat ctg aca ttc gcc gtg	1056
Val Arg Ser Pro Asp Ser Ala Cys Asn Pro Tyr Leu Thr Phe Ala Val	
340 345 350	
ctg ctg gcc gcg gga ttg cgg ggt gta gag aag ggt tac gtg ctg ggc	1104
Leu Leu Ala Ala Gly Leu Arg Gly Val Glu Lys Gly Tyr Val Leu Gly	
355 360 365	
ccg cag gcc gag gac aac gta tgg gac ctc aca ccc gag gaa cgc cga	1152
Pro Gln Ala Glu Asp Asn Val Trp Asp Leu Thr Pro Glu Glu Arg Arg	
370 375 380	
gcg atg ggg tac cga gaa ttg ccg tcc agt ttg gat agt gcg ctg cgc	1200
Ala Met Gly Tyr Arg Glu Leu Pro Ser Ser Leu Asp Ser Ala Leu Arg	
385 390 395 400	
gcc atg gag gcc tcc gaa ctc gtc gcg gag gcc ttg ggg gag cac gtt	1248
Ala Met Glu Ala Ser Glu Leu Val Ala Glu Ala Leu Gly Glu His Val	

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                405                410                415
ttt gac ttt ttc ttg cgc aac aag cgc acg gag tgg gcg aac tac cgc      1296
Phe Asp Phe Phe Leu Arg Asn Lys Arg Thr Glu Trp Ala Asn Tyr Arg
                420                425                430

agc cac gtc acg cca tac gag ctg cgc acc tac ctg tcg ctg tag      1341
Ser His Val Thr Pro Tyr Glu Leu Arg Thr Tyr Leu Ser Leu
                435                440                445

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<210> 10
<211> 446
<212> PRT
<213> Mycobacterium tuberculosis

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<220>
<221>
<222>
<223> Sequence is identical to SwissProt entry SP:GLN2_MYCTU
      Sequence is identical to PIR entry PIR:B70776

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<400> 10
Met Asp Arg Gln Lys Glu Phe Val Leu Arg Thr Leu Glu Glu Arg Asp
1          5          10          15

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Ile Arg Phe Val Arg Leu Trp Phe Thr Asp Val Leu Gly Phe Leu Lys
          20          25          30

```

```

Ser Val Ala Ile Ala Pro Ala Glu Leu Glu Gly Ala Phe Glu Glu Gly
          35          40          45

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Ile Gly Phe Asp Gly Ser Ser Ile Glu Gly Phe Ala Arg Val Ser Glu
50          55          60

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Ser Asp Thr Val Ala His Pro Asp Pro Ser Thr Phe Gln Val Leu Pro
65          70          75          80

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Trp Ala Thr Ser Ser Gly His His His Ser Ala Arg Met Phe Cys Asp
          85          90          95

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Ile Thr Met Pro Asp Gly Ser Pro Ser Trp Ala Asp Pro Arg His Val
          100          105          110

```

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Leu Arg Arg Gln Leu Thr Lys Ala Gly Glu Leu Gly Phe Ser Cys Tyr
          115          120          125

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Val His Pro Glu Ile Glu Phe Phe Leu Leu Lys Pro Gly Pro Glu Asp

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130	135	140
Gly Ser Val Pro Val Pro Val Asp Asn Ala Gly Tyr Phe Asp Gln Ala		
145	150	155 160
Val His Asp Ser Ala Leu Asn Phe Arg Arg His Ala Ile Asp Ala Leu		
	165	170 175
Glu Phe Met Gly Ile Ser Val Glu Phe Ser His His Glu Gly Ala Pro		
	180	185 190
Gly Gln Gln Glu Ile Asp Leu Arg Phe Ala Asp Ala Leu Ser Met Ala		
	195	200 205
Asp Asn Val Met Thr Phe Arg Tyr Val Ile Lys Glu Val Ala Leu Glu		
	210	215 220
Glu Gly Ala Arg Ala Ser Phe Met Pro Lys Pro Phe Gly Gln His Pro		
	225	230 235 240
Gly Ser Ala Met His Thr His Met Ser Leu Phe Glu Gly Asp Val Asn		
	245	250 255
Ala Phe His Ser Ala Asp Asp Pro Leu Gln Leu Ser Glu Val Gly Lys		
	260	265 270
Ser Phe Ile Ala Gly Ile Leu Glu His Ala Cys Glu Ile Ser Ala Val		
	275	280 285
Thr Asn Gln Trp Val Asn Ser Tyr Lys Arg Leu Val Gln Gly Gly Glu		
	290	295 300
Ala Pro Thr Ala Ala Ser Trp Gly Ala Ala Asn Arg Ser Ala Leu Val		
	305	310 315 320
Arg Val Pro Met Tyr Thr Pro His Lys Thr Ser Ser Arg Arg Val Glu		
	325	330 335
Val Arg Ser Pro Asp Ser Ala Cys Asn Pro Tyr Leu Thr Phe Ala Val		
	340	345 350
Leu Leu Ala Ala Gly Leu Arg Gly Val Glu Lys Gly Tyr Val Leu Gly		
	355	360 365

Pro Gln Ala Glu Asp Asn Val Trp Asp Leu Thr Pro Glu Glu Arg Arg
 370 375 380

Ala Met Gly Tyr Arg Glu Leu Pro Ser Ser Leu Asp Ser Ala Leu Arg
 385 390 395 400

Ala Met Glu Ala Ser Glu Leu Val Ala Glu Ala Leu Gly Glu His Val
 405 410 415

Phe Asp Phe Phe Leu Arg Asn Lys Arg Thr Glu Trp Ala Asn Tyr Arg
 420 425 430

Ser His Val Thr Pro Tyr Glu Leu Arg Thr Tyr Leu Ser Leu
 435 440 445

<210> 11
 <211> 1353
 <212> DNA
 <213> Mycobacterium tuberculosis

<220>
 <221> CDS
 <222> (1)..(1353)
 <223> Sequence is identical to nucleotides 4871-6223
 of GenBank entry GB:MTCY180 [Z97193]
 Sequence is identical to nucleotides 7308-8660
 of GenBank entry GB:AE007049

<400> 11
 atg aca gcc aca ccg ctt gcc gcg gcc gcg atc gcc caa ttg gag gca 48
 Met Thr Ala Thr Pro Leu Ala Ala Ala Ala Ile Ala Gln Leu Glu Ala
 1 5 10 15
 gag ggc gtc gac acc gtc atc ggc acc gtc gtg aac ccc gcc gga ctc 96
 Glu Gly Val Asp Thr Val Ile Gly Thr Val Val Asn Pro Ala Gly Leu
 20 25 30
 acc cag gcc aag acc gtg ccg ata cgc cgg acc aac aca ttc gcc aat 144
 Thr Gln Ala Lys Thr Val Pro Ile Arg Arg Thr Asn Thr Phe Ala Asn
 35 40 45
 cct ggc ctc ggc gcc agt ccg gtg tgg cat acc ttc tgt atc gac caa 192
 Pro Gly Leu Gly Ala Ser Pro Val Trp His Thr Phe Cys Ile Asp Gln
 50 55 60
 tgc agt att gca ttc acc gca gac atc agt gtg gtc ggc gat caa cgt 240
 Cys Ser Ile Ala Phe Thr Ala Asp Ile Ser Val Val Gly Asp Gln Arg
 65 70 75 80

ctc	cgc	atc	gat	ctg	tcc	gcc	ttg	cgc	atc	atc	ggc	gac	ggg	ttg	gcg	288
Leu	Arg	Ile	Asp	Leu	Ser	Ala	Leu	Arg	Ile	Ile	Gly	Asp	Gly	Leu	Ala	
				85					90					95		
tgg	gcg	ccc	gcc	ggg	ttc	ttc	gag	cag	gac	ggc	aca	ccg	gtc	ccc	gcc	336
Trp	Ala	Pro	Ala	Gly	Phe	Phe	Glu	Gln	Asp	Gly	Thr	Pro	Val	Pro	Ala	
			100					105					110			
tgc	agc	cga	gga	aca	ctg	agc	cgg	atc	gag	gcc	gcg	ctt	gct	gat	gcc	384
Cys	Ser	Arg	Gly	Thr	Leu	Ser	Arg	Ile	Glu	Ala	Ala	Leu	Ala	Asp	Ala	
		115					120					125				
ggc	atc	gac	gcg	gta	atc	ggc	cac	gaa	gtc	gaa	ttc	ctc	ttg	gtc	gac	432
Gly	Ile	Asp	Ala	Val	Ile	Gly	His	Glu	Val	Glu	Phe	Leu	Leu	Val	Asp	
	130					135					140					
gcg	gac	ggc	cag	cgg	ctg	cct	tcg	acg	ctg	tgg	gcg	cag	tac	ggg	gtc	480
Ala	Asp	Gly	Gln	Arg	Leu	Pro	Ser	Thr	Leu	Trp	Ala	Gln	Tyr	Gly	Val	
145					150					155					160	
gcc	ggg	gtg	ctc	gag	cac	gag	gcg	ttc	gtc	cgc	gat	gtc	aac	gcc	gcg	528
Ala	Gly	Val	Leu	Glu	His	Glu	Ala	Phe	Val	Arg	Asp	Val	Asn	Ala	Ala	
				165				170						175		
gca	acg	gca	gca	ggc	atc	gct	atc	gag	cag	ttc	cat	ccc	gaa	tac	ggg	576
Ala	Thr	Ala	Ala	Gly	Ile	Ala	Ile	Glu	Gln	Phe	His	Pro	Glu	Tyr	Gly	
			180					185					190			
gcc	aac	caa	ttc	gag	atc	tcg	tta	gcg	ccg	cag	ccg	ccg	gtc	gcg	gcc	624
Ala	Asn	Gln	Phe	Glu	Ile	Ser	Leu	Ala	Pro	Gln	Pro	Pro	Val	Ala	Ala	
		195					200					205				
gcc	gat	cag	ctg	gtg	ctg	acc	cgc	ctc	atc	atc	ggc	cgt	acc	gcc	cgc	672
Ala	Asp	Gln	Leu	Val	Leu	Thr	Arg	Leu	Ile	Ile	Gly	Arg	Thr	Ala	Arg	
	210					215					220					
cgg	cac	ggg	tta	cgc	gtg	agc	cta	tcg	cca	gcg	ccc	ttc	gcc	gga	agt	720
Arg	His	Gly	Leu	Arg	Val	Ser	Leu	Ser	Pro	Ala	Pro	Phe	Ala	Gly	Ser	
225					230				235					240		
atc	gga	tcc	ggg	gcc	cac	caa	cac	ttc	tcg	ctg	act	atg	tcg	gaa	ggg	768
Ile	Gly	Ser	Gly	Ala	His	Gln	His	Phe	Ser	Leu	Thr	Met	Ser	Glu	Gly	
				245				250						255		
atg	ctg	ttc	tcc	ggg	ggg	act	gga	gca	gct	ggc	atg	acc	tcg	gcc	ggg	816
Met	Leu	Phe	Ser	Gly	Gly	Thr	Gly	Ala	Ala	Gly	Met	Thr	Ser	Ala	Gly	
			260					265					270			
gag	gcc	gcg	gtg	gca	gga	gtg	ctt	cgc	gga	cta	ccg	gac	gcc	caa	ggc	864
Glu	Ala	Ala	Val	Ala	Gly	Val	Leu	Arg	Gly	Leu	Pro	Asp	Ala	Gln	Gly	
			275				280					285				
atc	ctg	tgc	gga	tcg	atc	gtg	tcc	ggg	ctg	cga	atg	cga	ccc	ggg	aac	912
Ile	Leu	Cys	Gly	Ser	Ile	Val	Ser	Gly	Leu	Arg	Met	Arg	Pro	Gly	Asn	
	290					295					300					
tgg	gcc	gga	atc	tat	gca	tgc	tgg	ggg	acc	gaa	aac	cgg	gaa	gcg	gcg	960

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Trp Ala Gly Ile Tyr Ala Cys Trp Gly Thr Glu Asn Arg Glu Ala Ala
305                      310                      315                      320

gtg cga ttc gtc aag ggc ggg gct ggc agc gcg tac ggc ggg aac gtg      1008
Val Arg Phe Val Lys Gly Gly Ala Gly Ser Ala Tyr Gly Gly Asn Val
                      325                      330                      335

gag gtg aag gtc gtc gac ccg tcg gcc aac ccg tat ctc gcg tcg gcg      1056
Glu Val Lys Val Val Asp Pro Ser Ala Asn Pro Tyr Leu Ala Ser Ala
                      340                      345                      350

gcg atc ctc gga ctg gca ctc gac ggc atg aag acc aag gcg gtg ttg      1104
Ala Ile Leu Gly Leu Ala Leu Asp Gly Met Lys Thr Lys Ala Val Leu
                      355                      360                      365

ccg tcg gaa acg acc gta gac ccg aca cag ctg tct gac gtg gat cgt      1152
Pro Ser Glu Thr Thr Val Asp Pro Thr Gln Leu Ser Asp Val Asp Arg
                      370                      375                      380

gac cgt gcc ggc att ctg cga ctt gct gcc gat cag gcg gat gca att      1200
Asp Arg Ala Gly Ile Leu Arg Leu Ala Ala Asp Gln Ala Asp Ala Ile
385                      390                      395                      400

gct gta ctg gat agt tcg aaa ctg ctt cgg tgc atc ctt ggc gat ccc      1248
Ala Val Leu Asp Ser Ser Lys Leu Leu Arg Cys Ile Leu Gly Asp Pro
                      405                      410                      415

gtg gta gat gcc gtg gtc gcg gta cgc cag tta gag cat gag cgc tac      1296
Val Val Asp Ala Val Val Ala Val Arg Gln Leu Glu His Glu Arg Tyr
                      420                      425                      430

ggg gac ctc gat cct gcg cag ctg gcc gac aag ttc cgg atg gct tgg      1344
Gly Asp Leu Asp Pro Ala Gln Leu Ala Asp Lys Phe Arg Met Ala Trp
435                      440                      445

agt gtg taa
Ser Val
450

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<210> 12
<211> 450
<212> PRT
<213> Mycobacterium tuberculosis

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<220>
<221>
<222>
<223> Sequence is identical to PIR entry PIR:C70515

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<400> 12
Met Thr Ala Thr Pro Leu Ala Ala Ala Ala Ile Ala Gln Leu Glu Ala
1                      5                      10                      15

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Glu Gly Val Asp Thr Val Ile Gly Thr Val Val Asn Pro Ala Gly Leu

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20	25	30
Thr Gln Ala Lys Thr Val Pro Ile Arg Arg Thr Asn Thr Phe Ala Asn		
35	40	45
Pro Gly Leu Gly Ala Ser Pro Val Trp His Thr Phe Cys Ile Asp Gln		
50	55	60
Cys Ser Ile Ala Phe Thr Ala Asp Ile Ser Val Val Gly Asp Gln Arg		
65	70	75
Leu Arg Ile Asp Leu Ser Ala Leu Arg Ile Ile Gly Asp Gly Leu Ala		
85	90	95
Trp Ala Pro Ala Gly Phe Phe Glu Gln Asp Gly Thr Pro Val Pro Ala		
100	105	110
Cys Ser Arg Gly Thr Leu Ser Arg Ile Glu Ala Ala Leu Ala Asp Ala		
115	120	125
Gly Ile Asp Ala Val Ile Gly His Glu Val Glu Phe Leu Leu Val Asp		
130	135	140
Ala Asp Gly Gln Arg Leu Pro Ser Thr Leu Trp Ala Gln Tyr Gly Val		
145	150	155
Ala Gly Val Leu Glu His Glu Ala Phe Val Arg Asp Val Asn Ala Ala		
165	170	175
Ala Thr Ala Ala Gly Ile Ala Ile Glu Gln Phe His Pro Glu Tyr Gly		
180	185	190
Ala Asn Gln Phe Glu Ile Ser Leu Ala Pro Gln Pro Pro Val Ala Ala		
195	200	205
Ala Asp Gln Leu Val Leu Thr Arg Leu Ile Ile Gly Arg Thr Ala Arg		
210	215	220
Arg His Gly Leu Arg Val Ser Leu Ser Pro Ala Pro Phe Ala Gly Ser		
225	230	235
Ile Gly Ser Gly Ala His Gln His Phe Ser Leu Thr Met Ser Glu Gly		
245	250	255

Met Leu Phe Ser Gly Gly Thr Gly Ala Ala Gly Met Thr Ser Ala Gly
 260 265 270

Glu Ala Ala Val Ala Gly Val Leu Arg Gly Leu Pro Asp Ala Gln Gly
 275 280 285

Ile Leu Cys Gly Ser Ile Val Ser Gly Leu Arg Met Arg Pro Gly Asn
 290 295 300

Trp Ala Gly Ile Tyr Ala Cys Trp Gly Thr Glu Asn Arg Glu Ala Ala
 305 310 315 320

Val Arg Phe Val Lys Gly Gly Ala Gly Ser Ala Tyr Gly Gly Asn Val
 325 330 335

Glu Val Lys Val Val Asp Pro Ser Ala Asn Pro Tyr Leu Ala Ser Ala
 340 345 350

Ala Ile Leu Gly Leu Ala Leu Asp Gly Met Lys Thr Lys Ala Val Leu
 355 360 365

Pro Ser Glu Thr Thr Val Asp Pro Thr Gln Leu Ser Asp Val Asp Arg
 370 375 380

Asp Arg Ala Gly Ile Leu Arg Leu Ala Ala Asp Gln Ala Asp Ala Ile
 385 390 395 400

Ala Val Leu Asp Ser Ser Lys Leu Leu Arg Cys Ile Leu Gly Asp Pro
 405 410 415

Val Val Asp Ala Val Val Ala Val Arg Gln Leu Glu His Glu Arg Tyr
 420 425 430

Gly Asp Leu Asp Pro Ala Gln Leu Ala Asp Lys Phe Arg Met Ala Trp
 435 440 445

Ser Val
 450

<210> 13
 <211> 1374
 <212> DNA

<213> Mycobacterium tuberculosis

<220>

<221> CDS

<222> (1) .. (1374)

<223> Sequence is identical to complement of nucleotides 3104-4477 of GenBank entry GB:MTV003 [AL008883]

Sequence is identical to complement of nucleotides 3138-4511 of GenBank entry GB:AE007117

<400> 13

gtg acc ggc ccc ggt tgc ccg ccg ttg gcg tgg acc gag ttg gag cga	48
Met Thr Gly Pro Gly Ser Pro Pro Leu Ala Trp Thr Glu Leu Glu Arg	
1 5 10 15	
ctg gtc gcg gcc ggt gac gtc gac acc gtc atc gtc gcg ttc acc gac	96
Leu Val Ala Ala Gly Asp Val Asp Thr Val Ile Val Ala Phe Thr Asp	
20 25 30	
atg cag ggc ccg ctg gcc ggc aaa ccg ata tgc ggc ccg cat ttc gtc	144
Met Gln Gly Arg Leu Ala Gly Lys Arg Ile Ser Gly Arg His Phe Val	
35 40 45	
gac gac ata gcc acc cgc ggc gtc gag tgc tgc agt tat ctg ctg gcc	192
Asp Asp Ile Ala Thr Arg Gly Val Glu Cys Cys Ser Tyr Leu Leu Ala	
50 55 60	
gtg gac gtc gac ctg aac acg gtg ccc ggc tat gcg atg gcc agt tgg	240
Val Asp Val Asp Leu Asn Thr Val Pro Gly Tyr Ala Met Ala Ser Trp	
65 70 75 80	
gac acc ggc tac ggc gat atg gtg atg acg ccg gac ttg tcc act ctg	288
Asp Thr Gly Tyr Gly Asp Met Val Met Thr Pro Asp Leu Ser Thr Leu	
85 90 95	
cgg ctg att cct tgg cta ccg gga acg gcg ctg gtg atc gcc gac ctg	336
Arg Leu Ile Pro Trp Leu Pro Gly Thr Ala Leu Val Ile Ala Asp Leu	
100 105 110	
gtc tgg gcc gac ggc agc gag gtc gcc gtc tgc ccg cgc agc att ctg	384
Val Trp Ala Asp Gly Ser Glu Val Ala Val Ser Pro Arg Ser Ile Leu	
115 120 125	
cgc cgt cag ctc gat cgg ctc aag gcg cgc gga ctg gtc gcc gat gtg	432
Arg Arg Gln Leu Asp Arg Leu Lys Ala Arg Gly Leu Val Ala Asp Val	
130 135 140	
gcc acc gag ctg gag ttc atc gtg ttc gac cag ccg tat cgc cag gca	480
Ala Thr Glu Leu Glu Phe Ile Val Phe Asp Gln Pro Tyr Arg Gln Ala	
145 150 155 160	
tgg gcc agc ggg tat cgc ggg ctg acc ccg gcc agc gac tac aac atc	528
Trp Ala Ser Gly Tyr Arg Gly Leu Thr Pro Ala Ser Asp Tyr Asn Ile	
165 170 175	
gac tac gcg ata ttg gca tcc tgc ccg atg gag ccg ttg ctg cgc gac	576

Asp Tyr Ala Ile Leu Ala Ser Ser Arg Met Glu Pro Leu Leu Arg Asp	
180 185 190	
atc cgg ttg ggt atg gcc ggt gcg ggt ctg cga ttc gag gcg gtc aaa	624
Ile Arg Leu Gly Met Ala Gly Ala Gly Leu Arg Phe Glu Ala Val Lys	
195 200 205	
ggc gaa tgc aac atg ggc cag cag gag atc ggg ttt cgt tac gac gag	672
Gly Glu Cys Asn Met Gly Gln Gln Glu Ile Gly Phe Arg Tyr Asp Glu	
210 215 220	
gcg ctg gtc acc tgc gac aac cat gcg atc tac aag aac ggc gcc aag	720
Ala Leu Val Thr Cys Asp Asn His Ala Ile Tyr Lys Asn Gly Ala Lys	
225 230 235 240	
gaa atc gcc gac cag cac ggc aag agc cta acg ttc atg gcg aaa tac	768
Glu Ile Ala Asp Gln His Gly Lys Ser Leu Thr Phe Met Ala Lys Tyr	
245 250 255	
gat gaa cgc gaa ggt aat agc tgt cac atc cat gtc tcg ctg cgt ggc	816
Asp Glu Arg Glu Gly Asn Ser Cys His Ile His Val Ser Leu Arg Gly	
260 265 270	
acg gat ggc tcc gcg gtg ttt gcc gac agt aac ggg ccg cac ggc atg	864
Thr Asp Gly Ser Ala Val Phe Ala Asp Ser Asn Gly Pro His Gly Met	
275 280 285	
tcg tcg atg ttc cgc agc ttc gtc gcc ggc cag ttg gcc acg ttg cgc	912
Ser Ser Met Phe Arg Ser Phe Val Ala Gly Gln Leu Ala Thr Leu Arg	
290 295 300	
gaa ttc acg ctg tgc tat gcg ccg acc att aac tcc tac aag cga ttt	960
Glu Phe Thr Leu Cys Tyr Ala Pro Thr Ile Asn Ser Tyr Lys Arg Phe	
305 310 315 320	
gcc gat agc agt ttc gcg ccg acg gcg ctg gct tgg ggg ctg gac aat	1008
Ala Asp Ser Ser Phe Ala Pro Thr Ala Leu Ala Trp Gly Leu Asp Asn	
325 330 335	
cgc acc tgc gcc ctg cgg gtg gtt ggc cac ggg caa aac atc cgg gtc	1056
Arg Thr Cys Ala Leu Arg Val Val Gly His Gly Gln Asn Ile Arg Val	
340 345 350	
gaa tgc cgg gtt ccc ggc ggt gat gtc aac cag tac ctg gcg gtg gcg	1104
Glu Cys Arg Val Pro Gly Gly Asp Val Asn Gln Tyr Leu Ala Val Ala	
355 360 365	
gct ctc att gct gga ggg ttg tac ggt atc gag cgg ggc ctt cag ctg	1152
Ala Leu Ile Ala Gly Gly Leu Tyr Gly Ile Glu Arg Gly Leu Gln Leu	
370 375 380	
ccc gag ccc tgt gtc ggc aac gcc tac caa ggc gcc gat gtc gaa cgg	1200
Pro Glu Pro Cys Val Gly Asn Ala Tyr Gln Gly Ala Asp Val Glu Arg	
385 390 395 400	
ctg ccg gtt acg ctg gcc gac gcc gcg gtg ctg ttc gag gat tct gcg	1248
Leu Pro Val Thr Leu Ala Asp Ala Ala Val Leu Phe Glu Asp Ser Ala	

405 410 415
 ctg gtg cgc gag gcg ttc ggc gag gat gtt gtc gcg cac tac ctg aac 1296
 Leu Val Arg Glu Ala Phe Gly Glu Asp Val Val Ala His Tyr Leu Asn
 420 425 430
 aac gcg cgt gtg gag ctg gcg gcg ttc aac gcg gcg gtc acc gat tgg 1344
 Asn Ala Arg Val Glu Leu Ala Ala Phe Asn Ala Ala Val Thr Asp Trp
 435 440 445
 gag agg ata cgt gga ttt gag gcg ctc tag 1374
 Glu Arg Ile Arg Gly Phe Glu Arg Leu
 450 455

 <210> 14
 <211> 457
 <212> PRT
 <213> Mycobacterium tuberculosis

 <220>
 <221>
 <222>
 <223> Sequence is identical to PIR entry PIR:F70885

 <400> 14
 Met Thr Gly Pro Gly Ser Pro Pro Leu Ala Trp Thr Glu Leu Glu Arg
 1 5 10 15

 Leu Val Ala Ala Gly Asp Val Asp Thr Val Ile Val Ala Phe Thr Asp
 20 25 30

 Met Gln Gly Arg Leu Ala Gly Lys Arg Ile Ser Gly Arg His Phe Val
 35 40 45

 Asp Asp Ile Ala Thr Arg Gly Val Glu Cys Cys Ser Tyr Leu Leu Ala
 50 55 60

 Val Asp Val Asp Leu Asn Thr Val Pro Gly Tyr Ala Met Ala Ser Trp
 65 70 75 80

 Asp Thr Gly Tyr Gly Asp Met Val Met Thr Pro Asp Leu Ser Thr Leu
 85 90 95

 Arg Leu Ile Pro Trp Leu Pro Gly Thr Ala Leu Val Ile Ala Asp Leu
 100 105 110

 Val Trp Ala Asp Gly Ser Glu Val Ala Val Ser Pro Arg Ser Ile Leu
 115 120 125

Arg Arg Gln Leu Asp Arg Leu Lys Ala Arg Gly Leu Val Ala Asp Val
 130 135 140

Ala Thr Glu Leu Glu Phe Ile Val Phe Asp Gln Pro Tyr Arg Gln Ala
 145 150 155 160

Trp Ala Ser Gly Tyr Arg Gly Leu Thr Pro Ala Ser Asp Tyr Asn Ile
 165 170 175

Asp Tyr Ala Ile Leu Ala Ser Ser Arg Met Glu Pro Leu Leu Arg Asp
 180 185 190

Ile Arg Leu Gly Met Ala Gly Ala Gly Leu Arg Phe Glu Ala Val Lys
 195 200 205

Gly Glu Cys Asn Met Gly Gln Gln Glu Ile Gly Phe Arg Tyr Asp Glu
 210 215 220

Ala Leu Val Thr Cys Asp Asn His Ala Ile Tyr Lys Asn Gly Ala Lys
 225 230 235 240

Glu Ile Ala Asp Gln His Gly Lys Ser Leu Thr Phe Met Ala Lys Tyr
 245 250 255

Asp Glu Arg Glu Gly Asn Ser Cys His Ile His Val Ser Leu Arg Gly
 260 265 270

Thr Asp Gly Ser Ala Val Phe Ala Asp Ser Asn Gly Pro His Gly Met
 275 280 285

Ser Ser Met Phe Arg Ser Phe Val Ala Gly Gln Leu Ala Thr Leu Arg
 290 295 300

Glu Phe Thr Leu Cys Tyr Ala Pro Thr Ile Asn Ser Tyr Lys Arg Phe
 305 310 315 320

Ala Asp Ser Ser Phe Ala Pro Thr Ala Leu Ala Trp Gly Leu Asp Asn
 325 330 335

Arg Thr Cys Ala Leu Arg Val Val Gly His Gly Gln Asn Ile Arg Val
 340 345 350

Glu Cys Arg Val Pro Gly Gly Asp Val Asn Gln Tyr Leu Ala Val Ala
355 360 365

Ala Leu Ile Ala Gly Gly Leu Tyr Gly Ile Glu Arg Gly Leu Gln Leu
370 375 380

Pro Glu Pro Cys Val Gly Asn Ala Tyr Gln Gly Ala Asp Val Glu Arg
385 390 395 400

Leu Pro Val Thr Leu Ala Asp Ala Ala Val Leu Phe Glu Asp Ser Ala
405 410 415

Leu Val Arg Glu Ala Phe Gly Glu Asp Val Val Ala His Tyr Leu Asn
420 425 430

Asn Ala Arg Val Glu Leu Ala Ala Phe Asn Ala Ala Val Thr Asp Trp
435 440 445

Glu Arg Ile Arg Gly Phe Glu Arg Leu
450 455